

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/777,145

Source: _____

Date Processed by STIC: _____

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/777,145

DATE: 10/18/2004

TIME: 10:11:54

Input Set : N:\CrF3\RULE60\10777145.raw.txt

Output Set: N:\CRF4\10182004\J777145.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Schlessinger, Joseph
6 Sap, Jan M.8 (ii) TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
9 PHOSPHATASE-ALPHA

11 (iii) NUMBER OF SEQUENCES: 14

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: PENNIE & EDMONDS
15 (B) STREET: 1155 AVENUE OF THE AMERICAS
16 (C) CITY: NEW YORK
17 (D) STATE: NEW YORK
18 (E) COUNTRY: U.S.A.
19 (F) ZIP: 10036

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/10/777,145
C--> 29 (B) FILING DATE: 13-Feb-2004
30 (C) CLASSIFICATION:

32 (vii) PRIOR APPLICATION DATA:

W--> 33 (A) APPLICATION NUMBER: US/09/280,597
34 (B) FILING DATE: 29-MAR-1999
W--> 35 (A) APPLICATION NUMBER: US 08/015,985
36 (B) FILING DATE: 10-FEB-1993

38 (viii) ATTORNEY/AGENT INFORMATION:

39 (A) NAME: Coruzzi, Laura A.
40 (B) REGISTRATION NUMBER: 30,742
41 (C) REFERENCE/DOCKET NUMBER: 7683-020

43 (ix) TELECOMMUNICATION INFORMATION:

44 (A) TELEPHONE: (212) 790-9090
45 (B) TELEFAX: (212) 869-9741/8864
46 (C) TELEX: 66141 PENNIE

50 (2) INFORMATION FOR SEQ ID NO: 1:

52 (i) SEQUENCE CHARACTERISTICS:

53 (A) LENGTH: 802 amino acids
54 (B) TYPE: amino acid
55 (D) TOPOLOGY: linear

57 (ii) MOLECULE TYPE: protein

59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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61 Met Asp Ser Trp Phe Ile Leu Val Leu Leu Gly Ser Gly Leu Ile Cys
 62 1 5 10 15
 64 Val Ser Ala Asn Asn Ala Thr Thr Val Ala Pro Ser Val Gly Ile Thr
 65 20 25 30
 67 Arg Leu Ile Asn Ser Ser Thr Ala Glu Pro Val Lys Glu Glu Ala Lys
 68 35 40 45
 70 Thr Ser Asn Pro Thr Ser Ser Leu Thr Ser Leu Ser Val Ala Pro Thr
 71 50 55 60
 73 Phe Ser Pro Asn Ile Thr Leu Gly Pro Thr Tyr Leu Thr Thr Val Asn
 74 65 70 75 80
 76 Ser Ser Asp Ser Asp Asn Gly Thr Thr Arg Thr Ala Ser Thr Asn Ser
 77 85 90 95
 79 Ile Gly Ile Thr Ile Ser Pro Asn Gly Thr Trp Leu Pro Asp Asn Gln
 80 100 105 110
 82 Phe Thr Asp Ala Arg Thr Glu Pro Trp Glu Gly Asn Ser Ser Thr Ala
 83 115 120 125
 85 Ala Thr Thr Pro Glu Thr Phe Pro Pro Ser Gly Asn Ser Asp Ser Lys
 86 130 135 140
 88 Asp Arg Arg Asp Glu Thr Pro Ile Ile Ala Val Met Val Ala Leu Ser
 89 145 150 155 160
 91 Ser Leu Leu Val Ile Val Phe Ile Ile Val Leu Tyr Met Leu Arg
 92 165 170 175
 94 Phe Lys Lys Tyr Lys Gln Ala Gly Ser His Ser Asn Ser Phe Arg Leu
 95 180 185 190
 97 Ser Asn Gly Arg Thr Glu Asp Val Glu Pro Gln Ser Val Pro Leu Leu
 98 195 200 205
 100 Ala Arg Ser Pro Ser Thr Asn Arg Lys Tyr Pro Pro Leu Pro Val Asp
 101 210 215 220
 103 Lys Leu Glu Glu Glu Ile Asn Arg Arg Met Ala Asp Asp Asn Lys Leu
 104 225 230 235 240
 106 Phe Arg Glu Glu Phe Asn Ala Leu Pro Ala Cys Pro Ile Gln Ala Thr
 107 245 250 255
 109 Cys Glu Ala Ala Ser Lys Glu Glu Asn Lys Glu Lys Asn Arg Tyr Val
 110 260 265 270
 112 Asn Ile Leu Pro Tyr Asp His Ser Arg Val His Leu Thr Pro Val Glu
 113 275 280 285
 115 Gly Val Pro Asp Ser Asp Tyr Ile Asn Ala Ser Phe Ile Asn Gly Tyr
 116 290 295 300
 118 Gln Glu Lys Asn Lys Phe Ile Ala Ala Gln Gly Pro Lys Glu Glu Thr
 119 305 310 315 320
 121 Val Asn Asp Phe Trp Arg Met Ile Trp Glu Gln Asn Thr Ala Thr Ile
 122 325 330 335
 124 Val Met Val Thr Asn Leu Lys Glu Arg Lys Glu Cys Lys Cys Ala Gln
 125 340 345 350
 127 Tyr Trp Pro Asp Gln Gly Cys Trp Thr Tyr Gly Asn Ile Arg Val Ser
 128 355 360 365
 130 Val Glu Asp Val Thr Val Leu Val Asp Tyr Thr Val Arg Lys Phe Cys
 131 370 375 380
 133 Ile Gln Gln Val Gly Asp Met Thr Asn Arg Lys Pro Gln Arg Leu Ile

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134	385	390	395	400
136	Thr Gln Phe His Phe Thr Ser Trp Pro Asp Phe Gly Val Pro Phe Thr			
137		405	410	415
139	Pro Ile Gly Met Leu Lys Phe Leu Lys Lys Val Lys Ala Cys Asn Pro			
140		420	425	430
142	Gln Tyr Ala Gly Ala Ile Val Val His Cys Ser Ala Gly Val Gly Arg			
143		435	440	445
145	Thr Gly Thr Phe Val Val Ile Asp Ala Met Leu Asp Met Met His Thr			
146		450	455	460
148	Glu Arg Lys Val Asp Val Tyr Gly Phe Val Ser Arg Ile Arg Ala Gln			
149		465	470	475
151	Arg Cys Gln Met Val Gln Thr Asp Met Gln Tyr Val Phe Ile Tyr Gln			
152		485	490	495
154	Ala Leu Leu Glu His Tyr Leu Tyr Gly Asp Thr Glu Leu Glu Val Thr			
155		500	505	510
157	Ser Leu Glu Thr His Leu Gln Lys Ile Tyr Asn Lys Ile Pro Gly Thr			
158		515	520	525
160	Ser Asn Asn Gly Leu Glu Glu Phe Lys Lys Leu Thr Ser Ile Lys			
161		530	535	540
163	Ile Gln Asn Asp Lys Met Arg Thr Gly Asn Leu Pro Ala Asn Met Lys			
164		545	550	555
166	Lys Asn Arg Val Leu Gln Ile Ile Pro Tyr Glu Phe Asn Arg Val Ile			
167		565	570	575
169	Ile Pro Val Lys Arg Gly Glu Asn Thr Asp Tyr Val Asn Ala Ser			
170		580	585	590
172	Phe Ile Asp Gly Tyr Arg Gln Lys Asp Ser Tyr Ile Ala Ser Gln Gly			
173		595	600	605
175	Pro Leu Leu His Thr Ile Glu Asp Phe Trp Arg Met Ile Trp Glu Trp			
176		610	615	620
178	Lys Ser Cys Ser Ile Val Met Leu Thr Glu Leu Glu Glu Arg Gly Gln			
179		625	630	635
181	Glu Lys Cys Ala Gln Tyr Trp Pro Ser Asp Gly Leu Val Ser Tyr Gly			
182		645	650	655
184	Asp Ile Thr Val Glu Leu Lys Glu Glu Glu Cys Glu Ser Tyr Thr			
185		660	665	670
187	Val Arg Asp Leu Leu Val Thr Asn Thr Arg Glu Asn Lys Ser Arg Gln			
188		675	680	685
190	Ile Arg Gln Phe His Phe His Gly Trp Pro Glu Val Gly Ile Pro Ser			
191		690	695	700
193	Asp Gly Lys Gly Met Ile Ser Ile Ile Ala Ala Val Gln Lys Gln Gln			
194		705	710	715
196	Gln Gln Ser Gly Asn His Pro Ile Thr Val His Cys Ser Ala Gly Ala			
197		725	730	735
199	Gly Arg Thr Gly Thr Phe Cys Ala Leu Ser Thr Val Leu Glu Arg Val			
200		740	745	750
202	Lys Ala Glu Gly Ile Leu Asp Val Phe Gln Thr Val Lys Ser Leu Arg			
203		755	760	765
205	Leu Gln Arg Pro His Met Val Gln Thr Leu Glu Gln Tyr Glu Phe Cys			
206		770	775	780

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208 Tyr Lys Val Val Gln Glu Tyr Ile Asp Ala Phe Ser Asp Tyr Ala Asn
209 785 790 795 800

211 Phe Lys

214 (2) INFORMATION FOR SEQ ID NO: 2:

216 (i) SEQUENCE CHARACTERISTICS:

- 217 (A) LENGTH: 2409 base pairs
- 218 (B) TYPE: nucleic acid
- 219 (C) STRANDEDNESS: double
- 220 (D) TOPOLOGY: unknown

222 (ii) MOLECULE TYPE: cDNA

224 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

226 ATGGATTCCCT	GGTTCATTCCT	TGTTCTGCTC	GGCAGTGGTC	TGATATGTGT	CAGTGCCAAC	60
228 AATGCTACCA	CAGTTGCACC	TTCTGTAGGA	ATTACAAGAT	TAATTAACTC	ATCAACGGCA	120
230 GAACCAGTTA	AAGAACAGGC	CAAAACTTCA	AATCCAACCTT	CTTCACTAAC	TTCTCTTCT	180
232 GTGGCACCAA	CATTCAAGCCC	AAATAATAACT	CTGGGACCCA	CCTATTAAAC	CACTGTCAAT	240
234 TCTTCAGACT	CTGACAATGG	GACCACAAGA	ACAGCAAGCA	CCAATTCTAT	AGGCATTACA	300
236 ATTTCACCAA	ATGGAACGTG	GCTTCCAGAT	AACCAGTTCA	CGGATGCCAG	AACAGAACCC	360
238 TGGGAGGGGA	ATTCCAGCAC	CGCAGCAACC	ACTCCAGAAA	CTTCCCTCC	TTCAGGTAAT	420
240 TCTGACTCGA	AGGACAGAAC	AGATGAGACA	CCAATTATTG	CGGTGATGGT	GGCCCTGTCC	480
242 TCTCTGCTAG	TGATCGTGT	TATTATCATA	GTGTTGTACA	TGTTAAGGTT	TAAGAAATAC	540
244 AAGCAAGCTG	GGAGCCATT	CAATTCTTTC	CGCTTATCCA	ACGGCCGCAC	TGAGGATGTG	600
246 GAGCCCCAGA	GTGTGCCACT	TCTGGCCAGA	TCCCCAAGCA	CCAACAGGAA	ATACCCACCC	660
248 CTGCCCGTGG	ACAAGCTGGA	AGAGGAAATT	AACCGGAGAA	TGGCAGACGA	CAATAAGCTC	720
250 TTCAGGGAGG	AATTCAACGC	TCTCCCTGCA	TGTCCTATCC	AGGCCACCTG	TGAGGCTGCT	780
252 TCCAAGGAGG	AAAACAAGGA	AAAAAAATCGA	TATGTAAACA	TCTTGCCTTA	TGACCACTCT	840
254 AGAGTCCACC	TGACACCGGT	TGAAGGGTT	CCAGATTCTG	ATTACATCAA	TGCTTCATTC	900
256 ATCAACGGTT	ACCAAGAAAA	GAACAAATTC	ATTGCTGCAC	AAGGACAAA	AGAAGAACG	960
258 GTGAATGATT	TCTGGCGGAT	GATCTGGAA	CAAAACACAG	CCACCATCGT	CATGGTTACC	1020
260 AACCTGAAGG	AGAGAAAGGA	GTGCAAGTGC	GCCCAGTACT	GGCCAGACCA	AGGCTGCTGG	1080
262 ACCTATGGGA	ATATTCCGGT	GTCCTGTAGAG	GATGTGACTG	TCCTGGTGG	CTACACAGTA	1140
264 CGGAAGTTCT	GCATCCAGCA	GGTGGCGAC	ATGACCAACA	GAAAGCCACA	GCGCCTCATC	1200
266 ACTCAGTTCC	ACTTTACCA	CTGGCCAGAC	TTTGGGGTGC	CTTTTACCCC	GATCGGCATG	1260
268 CTCAGTTCC	TCAAGAAGGT	GAAGGCCCTGT	AACCCCTAGT	ATGCAGGGC	CATCGTGGTC	1320
270 CACTGCAGTG	CAGGTGTTAGG	GGTACAGGT	ACCTTTGTCG	TCATTGATGC	CATGCTGGAC	1380
272 ATGATGCATA	CAGAACGGAA	GGTGGACGTG	TATGGCTTTG	TGAGCCGGAT	CCGGGCACAG	1440
274 CGCTGCCAGA	TGGTGCAAAC	CGATATGCAG	TATGTCTTCA	TATACCAAGC	CCTCTGGAG	1500
276 CATTATCTCT	ATGGAGATAC	AGAACTGGAA	GTGACCTCTC	TAGAAACCCA	CCTGCAGAAA	1560
278 ATTTACAACA	AAATCCCAGG	GACCAGCAAC	AATGGATTAG	AGGAGGAGTT	TAAGAAGTTA	1620
280 ACATCAATCA	AAATCCAGAA	TGACAAGATG	CGGACTGGAA	ACCTTCCAGC	CAACATGAAG	1680
282 AAGAACCGTG	TTTTACAGAT	CATTCCATAT	GAATTCAACA	GAGTGTACAT	TCCAGTTAAG	1740
284 CGGGGCGAAG	AGAATACAGA	CTATGTGAAC	GCATCCTTA	TTGATGGCTA	CCGGCAGAAG	1800
286 GACTCCTATA	TCGCCAGCCA	GGGCCCTCTT	CTCCACACAA	TTGAGGACTT	CTGGCGAATG	1860
288 ATCTGGGAGT	GGAAATCCTG	CTCTATCGT	ATGCTAACAG	AACTGGAGGA	GAGAGGCCAG	1920
290 GAGAAGTGTG	CCCAGTACTG	GCCATCTGAT	GGACTGGTGT	CCTATGGAGA	TATTACAGTG	1980
292 GAACTGAAGA	AGGAGGAGGA	ATGTGAGAGC	TACACCGTCC	GAGACCTCCT	GGTCACCAAC	2040
294 ACCAGGGAGA	ATAAGAGCCG	GCAGATCCGG	CAGTCCACT	TCCATGGCTG	GCCTGAAGTG	2100
296 GGCATCCCCA	GTGACGGAAA	GGGCATGATC	AGCATCATCG	CCGCCGTGCA	GAAGCAGCAG	2160
298 CAGCAGTCAG	GGAACCAACC	CATCACCGTG	CACTGCAGCG	CCGGGGCAGG	AAGGACGGGG	2220
300 ACCTTCTGTG	CCCTGAGCAC	CGTCCTGGAG	CGTGTGAAAG	CAGAGGGGAT	TTTGGATGTC	2280

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302	TTCCAGACTG	TCAAGAGCCT	GCGGCTACAG	AGGCCACACA	TGGTCCAGAC	ACTGGAACAG	2340
304	TATGAGTTCT	GCTACAAGGT	GGTGCAGGAG	TATATTGATG	CATTCTCAGA	TTATGCCAAC	2400
306	TTCAAGTAA						2409
309	(2) INFORMATION FOR SEQ ID NO: 3:						
311	(i) SEQUENCE CHARACTERISTICS:						
312	(A) LENGTH: 793 amino acids						
313	(B) TYPE: amino acid						
314	(D) TOPOLOGY: linear						
316	(ii) MOLECULE TYPE: protein						
318	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:						
320	Met Asp Ser Trp Phe Ile Leu Val Leu Phe Gly Ser Gly Leu Ile His						
321	1	5	10	15			
323	Val Ser Ala Asn Asn Ala Thr Thr Val Ser Pro Ser Leu Gly Thr Thr						
324	20	25	30				
326	Arg Leu Ile Lys Thr Ser Thr Thr Glu Leu Ala Lys Glu Glu Asn Lys						
327	35	40	45				
329	Thr Ser Asn Ser Thr Ser Ser Val Ile Ser Leu Ser Val Ala Pro Thr						
330	50	55	60				
332	Phe Ser Pro Asn Leu Thr Leu Glu Pro Thr Tyr Val Thr Thr Val Asn						
333	65	70	75	80			
335	Ser Ser His Ser Asp Asn Gly Thr Arg Arg Ala Ala Ser Thr Glu Ser						
336	85	90	95				
338	Gly Gly Thr Thr Ile Ser Pro Asn Gly Ser Trp Leu Ile Glu Asn Gln						
339	100	105	110				
341	Phe Thr Asp Ala Ile Thr Glu Pro Trp Glu Gly Asn Ser Ser Thr Ala						
342	115	120	125				
344	Ala Thr Thr Pro Glu Thr Phe Pro Pro Ala Asp Glu Thr Pro Ile Ile						
345	130	135	140				
347	Ala Val Met Val Ala Leu Ser Ser Leu Leu Val Ile Val Phe Ile Ile						
348	145	150	155	160			
350	Ile Val Leu Tyr Met Leu Arg Phe Lys Lys Tyr Lys Gln Ala Gly Ser						
351	165	170	175				
353	His Ser Asn Ser Phe Arg Leu Ser Asn Gly Arg Thr Glu Asp Val Glu						
354	180	185	190				
356	Pro Gln Ser Val Pro Leu Leu Ala Arg Ser Pro Ser Thr Asn Arg Lys						
357	195	200	205				
359	Tyr Pro Pro Leu Pro Val Asp Lys Leu Glu Glu Glu Ile Asn Arg Arg						
360	210	215	220				
362	Met Ala Asp Asp Asn Lys Leu Phe Arg Glu Glu Phe Asn Ala Leu Pro						
363	225	230	235	240			
365	Ala Cys Pro Ile Gln Ala Thr Cys Glu Ala Ala Ser Lys Glu Glu Asn						
366	245	250	255				
368	Lys Glu Lys Asn Arg Tyr Val Asn Ile Leu Pro Tyr Asp His Ser Arg						
369	260	265	270				
371	Val His Leu Thr Pro Val Glu Gly Val Pro Asp Ser Asp Tyr Ile Asn						
372	275	280	285				
374	Ala Ser Phe Ile Asn Gly Tyr Gln Glu Lys Asn Lys Phe Ile Ala Ala						
375	290	295	300				
377	Gln Gly Pro Lys Glu Glu Thr Val Asn Asp Phe Trp Arg Met Ile Trp						

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 10/18/2004
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; Xaa Pos.8,12,21,22,24,25,27,28,30,37,39,47,57,72,77,89,94,95,99,104
Seq#:9; Xaa Pos.109,111,115,116,124,125,131,133,135,137,138,139,143,144,153
Seq#:9; Xaa Pos.155,170,174,176,179,180,181,182,183,186,205,211,212,214,215
Seq#:9; Xaa Pos.217,222,227,230,232,240,244,247
Seq#:14; Xaa Pos.10,20,21,22,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38
Seq#:14; Xaa Pos.39,40,41,42,43,55,67,70,87,95,96,97,99,100,103,105,106,112
Seq#:14; Xaa Pos.114,115,116,120,121,123,126,127,128,133,137,138,139,141
Seq#:14; Xaa Pos.143,149,151,182,186,188,195,196,197,198,199,200,201,202
Seq#:14; Xaa Pos.205,209,212,213,214,218,222,224,228,229,244,247,254,257
Seq#:14; Xaa Pos.264,265,266,267

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10777145.raw.txt

Output Set: N:\CRF4\10182004\J777145.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:35 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)
L:836 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
M:341 Repeated in SeqNo=9
L:1142 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
M:341 Repeated in SeqNo=14